

**Poster 2. Development, mapping, and haplotype analysis of EST-based SNPs for wheat *Fusarium* head blight resistance QTL *Fhb1*.**

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*Fusarium* head blight (FHB) is a destructive disease that reduces wheat grain yield and quality. The Chinese variety Sumai3 and its derivatives such as Ning 7840 have a high level of resistance to FHB symptom spread within a spike (type-II resistance) and have been widely used as resistant parents in breeding programs worldwide. The quantitative trait locus (QTL) in chromosome 3BS (*Fhb1*) from Sumai3 has been identified to have the largest effect on FHB resistance to date. This QTL has been linked to restriction fragment length polymorphism, simple sequence repeat (SSR), amplified fragment length polymorphism, and sequence tagged site (STS) markers. Single nucleotide polymorphism (SNP) is the most common form of genetic variation, and SNP may be the next generation marker system for mapping and marker-assisted selection (MAS). In this study, we developed SNP markers based on wheat expressed sequence tags (ESTs) associated with the 3BS QTL region. A total of 131 SNPs were identified between Ning 7840 (FHB resistant) and Clark (susceptible) based on the sequences of ten ESTs. SNPs were analyzed in 71 'Ning 7840/Clark' BC<sub>7</sub>F<sub>7</sub> populations using the single-base extension method. Seven SNP markers mapped between *Xgwm533* and *Xgwm493*; SSR markers flanking *Fhb1* in 3BS. Five of these SNP markers clustered with four other SSR/STS markers and covered a 7.4-cM interval, 12.9 cM from *Xgwm533*. This marker-dense region gave the highest R<sup>2</sup> (40–54%) and LOD values (9.16–11.80) and is the most likely location of *Fhb1*. Haplotype analysis of 63 lines from eight countries based on EST sequence (SNP), SSR, and STS markers associated with *Fhb1* identified four major groups: (1) Clark, (2) Asian, (3) Ernie, and (4) Chinese Spring. The Asian group consisted of Chinese and Japanese lines that carry the *Fhb1* resistance QTL and one *Xsnp-11* marker haplotype could differentiate these lines from lines in other groups. All Sumai3-related lines formed a subcluster within the Asian group, and an *Xsnp3BS-8* marker haplotype is specific for these lines. The SNP markers identified in this study should be useful for fine-mapping and MAS of *Fhb1*.

**Poster 3. The International Wheat Genome Sequencing Consortium: a genome sequence-based platform to accelerate wheat improvement.**

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Bread wheat is grown on over 95% of the wheat-growing area, and its sequence holds the key to genetic improvements necessary to meet the increasing demands for high-quality food and feed produced in an environmentally sensitive, sustainable, and profitable manner. Furthermore, because of its recent history, hexaploid wheat is a very good model to study polyploidy, a driving force for plant genome evolution. The International Wheat Genome Sequencing Consortium (IWGSC) was established by plant scientists, breeders, and growers who are dedicated to sequencing the wheat genome to enhance our knowledge of its structure and function and deploy state-of-the-art molecular tools to accelerate wheat improvement and meet the challenges of the 21st century. The Consortium is committed to ensuring that the wheat genome sequence, and the resulting DNA-based tools are available for all to use without restriction. To achieve the vision of a sequenced wheat genome, the IWGSC develops strategic plans with short- and mid-term goals; defines areas of coordination; facilitates and coordinates research projects and funding efforts at the national and international levels; develops and supports the design of research proposals; provides a framework for the establishment of common guidelines, protocols, and resources; and organizes scientific meetings and workshops. The IWGSC is governed by six co-chairs, a Coordinating Committee, and an executive director. General membership is open to any individual, laboratory, or entity with an active interest in meeting IWGSC objectives. The mission, goals, organizational structure, projects, and online membership registration are available at <http://www.wheatgenome.org>.